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RAW SEQUENCE LISTING

DATE: 01/21/2004

PATENT APPLICATION: US/10/644,875

TIME: 14:50:31

Input Set : N:\Crf3\RULE60\10644875.RAW.txt

Output Set: N:\CRF4\01212004\J644875.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Wei, et al.

7 (ii) TITLE OF INVENTION: Transforming Growth Factor Alpha HII

9 (iii) NUMBER OF SEQUENCES: 14

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Human Genome Sciences, Inc.

13 (B) STREET: 9410 Key West Ave

14 (C) CITY: Rockville

15 (D) STATE: MD

16 (E) COUNTRY: US

17 (F) ZIP: 20850

19 (v) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

21 (B) COMPUTER: IBM PC compatible

22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

C--> 26 (A) APPLICATION NUMBER: US/10/644,875

C--> 27 (B) FILING DATE: 21-Aug-2003

28 (C) CLASSIFICATION: 536

C--> 37 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/09/227,853A

32 (B) FILING DATE: 11-JAN-1999

34 (A) APPLICATION NUMBER: 08/930,564

35 (B) FILING DATE: 30-JAN-1998

38 (A) APPLICATION NUMBER: WO PCT/US95/06386

39 (B) FILING DATE: 19-MAY-1995

C--> 41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Brookes, A. Anders

43 (B) REGISTRATION NUMBER: 36,373

44 (C) REFERENCE/DOCKET NUMBER: PF174USD1

C--> 46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: 301-309-8504

48 (B) TELEFAX: 301-309-8439

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1695 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: single

57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: DNA (genomic)

62 (ix) FEATURE:

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63      (A) NAME/KEY: CDS
64      (B) LOCATION: 323..1444
65
66      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67
68      CACTCGTCTG CCCCTGGACT CCCGTCTCCT CCTGTCTCTCC GGCTTCCCAG AGCTCCCCTCC      60
69      TTATGGCAGC AGCTTCCCAG GTCTCCGGCG CAGTTCTCAG CGGACGACCC TCTCGCTCCG      120
70      GGGCTGAGCC CAGTCCCTGG ATGTTGCTGA AACTCTCGAG ATCATGCGCG GGTTTGGCTG      180
71      CTGCTTCCCC GCCGGGTGCC ACTGCCACCG CCGCCGCCCTC TGCTGCCGCC GTCCGCGGGA      240
72      TGCTCAGTAG CCCGCTGCCC GGCCCCGCG ATCCTGTGTT CCTCGGAAGC CGTTTGCTGC      300
73      TGCAGAGTTG CACGAAGTAG TC ATG GTG CTG TGG GAG TCC CCG CGG CAG TGC      352
74
75      Met Val Leu Trp Glu Ser Pro Arg Gln Cys
76      1 5 10
77
78      AGC AGC TGG ACA CTT TGC GAG GGC TTT TGC TGG CTG CTG CTG CTG CCC      400
79      Ser Ser Trp Thr Leu Cys Glu Gly Phe Cys Trp Leu Leu Leu Leu Pro
80      15 20 25
81      GTC ATG CTA CTC ATC GTA GCC CGC CCG GTG AAG CTC GCT GCT TTC CCT      448
82      Val Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro
83      30 35 40
84      ACC TCC TTA AGT GAC TGC CAA ACG CCC ACC GGC TGG AAT TGC TCT GGT      496
85      Thr Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly
86      45 50 55
87      TAT GAT GAC AGA GAA AAT GAT CTC TTC CTC TGT GAC ACC AAC ACC TGT      544
88      Tyr Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys
89      60 65 70
90      AAA TTT GAT GGG GAA TGT TTA AGA ATT GGA GAC ACT GTG ACT TGC GTC      592
91      Lys Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val
92      75 80 85 90
93      TGT CAG TTC AAG TGC AAC AAT GAC TAT GTG CCT GTG TGT GGC TCC AAT      640
94      Cys Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn
95      95 100 105
96      GGG GAG AGC TAC CAG AAT GAG TGT TAC CTG CGA CAG GCT GCA TGC AAA      688
97      Gly Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys
98      110 115 120
99      CAG CAG AGT GAG ATA CTT GTG GTG TCA GAA GGA TCA TGT GCC ACA GAT      736
100      Gln Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp
101      125 130 135
102      GCA GGA TCA GGA TCT GGA GAT GGA GTC CAT GAA GGC TCT GGA GAA ACT      784
103      Ala Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr
104      140 145 150
105      AGT CAA AAG GAG ACA TCC ACC TGT GAT ATT TGC CAG TTT GGT GCA GAA      832
106      Ser Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu
107      155 160 165 170
108      TGT GAC GAA GAT GCC GAG GAT GTC TGG TGT GTG TGT AAT ATT GAC TGT      880
109      Cys Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys
110      175 180 185
111      TCT CAA ACC AAC TTC AAT CCC CTC TGC GCT TCT GAT GGG AAA TCT TAT      928
112      Ser Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr
113      190 195 200
114      GAT AAT GCA TGC CAA ATC AAA GAA GCA TCG TGT CAG AAA CAG GAG AAA      976
115      Asp Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys

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134          205          210          215
136 ATT GAA GTC ATG TCT TTG GGT CGA TGT CAA GAT AAC ACA ACT ACA ACT      1024
137 Ile Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr
138          220          225          230
140 ACT AAG TCT GAA GAT GGG CAT TAT GCA AGA ACA GAT TAT GCA GAG AAT      1072
141 Thr Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn
142 235          240          245          250
144 GCT AAC AAA TTA GAA GAA AGT GCC AGA GAA CAC ATA CCT TGT CCG      1120
145 Ala Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro
146          255          260          265
148 GAA CAT TAC AAT GGC TTC TGC ATG CAT GGG AAG TGT GAG CAT TCT ATC      1168
149 Glu His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile
150          270          275          280
152 AAT ATG CAG GAG CCA TCT TGC AGG TGT GAT GCT GGT TAT ACT GGA CAA      1216
153 Asn Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln
154          285          290          295
156 CAC TGT GAA AAA AAG GAC TAC AGT GTT CTA TAC GTT GTT CCC GGT CCT      1264
157 His Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro
158          300          305          310
160 GTA CGA TTT CAG TAT GTC TTA ATC GCA GCT GTG ATT GGA ACA ATT CAG      1312
161 Val Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln
162 315          320          325          330
164 ATT GCT GTC ATC TGT GTG GTG GTC CTC TGC ATC ACA AGG AAA TGC CCC      1360
165 Ile Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro
166          335          340          345
168 AGA AGC AAC AGA ATT CAC AGA CAG AAG CAA AAT ACA GGG CAC TAC AGT      1408
169 Arg Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser
170          350          355          360
172 TCG GAC AAT ACA ACA AGA GCG TCC ACG AGG TTA ATC TAAAGGGAGC      1454
173 Ser Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile
174          365          370
176 ATGTTTCACA GTGGCTGGAC TACCGAGAGC TTGGACTACA CAATACAGTA TTATAGACAA      1514
178 AAGAATAAGA CAAGAGATCT ACACATGTTG CCTTGCATTT GTGGTAATCT ACACCAATGA      1574
180 AAACATGTAC TACAGCTATA TTTGATTATG TATGGATATA TTTGAAATAG TATACATTGT      1634
182 CTTGATGTTT TTTCTGTAAT GTAAATAAAC TATTTATATC ACACAAAAAA AAAAAAAA      1694
184 A      1695
187 (2) INFORMATION FOR SEQ ID NO: 2:
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 374 amino acids
191 (B) TYPE: amino acid
192 (D) TOPOLOGY: linear
194 (ii) MOLECULE TYPE: protein
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
198 Met Val Leu Trp Glu Ser Pro Arg Gln Cys Ser Ser Trp Thr Leu Cys
199 1          5          10          15
201 Glu Gly Phe Cys Trp Leu Leu Leu Leu Pro Val Met Leu Leu Ile Val
202          20          25          30
204 Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr Ser Leu Ser Asp Cys
205          35          40          45

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207 Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr Asp Asp Arg Glu Asn
208      50                      55                      60
210 Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys Phe Asp Gly Glu Cys
211 65                      70                      75                      80
213 Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys Gln Phe Lys Cys Asn
214                      85                      90                      95
216 Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly Glu Ser Tyr Gln Asn
217                      100                      105                      110
219 Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln Gln Ser Glu Ile Leu
220                      115                      120                      125
222 Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala Gly Ser Gly Ser Gly
223                      130                      135                      140
225 Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser Gln Lys Glu Thr Ser
226 145                      150                      155                      160
228 Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys Asp Glu Asp Ala Glu
229                      165                      170                      175
231 Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser Gln Thr Asn Phe Asn
232                      180                      185                      190
234 Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp Asn Ala Cys Gln Ile
235                      195                      200                      205
237 Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile Glu Val Met Ser Leu
238                      210                      215                      220
240 Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr Lys Ser Glu Asp Gly
241 225                      230                      235                      240
243 His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala Asn Lys Leu Glu Glu
244                      245                      250                      255
246 Ser Ala Arg Glu His His Ile Pro Cys Pro Glu His Tyr Asn Gly Phe
247                      260                      265                      270
249 Cys Met His Gly Lys Cys Glu His Ser Ile Asn Met Gln Glu Pro Ser
250                      275                      280                      285
252 Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His Cys Glu Lys Lys Asp
253                      290                      295                      300
255 Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val Arg Phe Gln Tyr Val
256 305                      310                      315                      320
258 Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile Ala Val Ile Cys Val
259                      325                      330                      335
261 Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg Ser Asn Arg Ile His
262                      340                      345                      350
264 Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser Asp Asn Thr Thr Arg
265                      355                      360                      365
267 Ala Ser Thr Arg Leu Ile
268                      370

```

270 (2) INFORMATION FOR SEQ ID NO: 3:

272 (i) SEQUENCE CHARACTERISTICS:

273 (A) LENGTH: 30 base pairs

274 (B) TYPE: nucleic acid

275 (C) STRANDEDNESS: single

276 (D) TOPOLOGY: linear

278 (ii) MOLECULE TYPE: DNA (genomic)

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Output Set: N:\CRF4\01212004\J644875.raw

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283      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
285 CCCGGATCCG CACGAGACAT ACCTTGTCCTG      30
287 (2) INFORMATION FOR SEQ ID NO: 4:
289      (i) SEQUENCE CHARACTERISTICS:
290          (A) LENGTH: 32 base pairs
291          (B) TYPE: nucleic acid
292          (C) STRANDEDNESS: single
293          (D) TOPOLOGY: linear
295      (ii) MOLECULE TYPE: DNA (genomic)
300      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
302 GGGAAGCTTT TAATACTGAA ATCGTACAGG AC      32
304 (2) INFORMATION FOR SEQ ID NO: 5:
306      (i) SEQUENCE CHARACTERISTICS:
307          (A) LENGTH: 33 base pairs
308          (B) TYPE: nucleic acid
309          (C) STRANDEDNESS: single
310          (D) TOPOLOGY: linear
312      (ii) MOLECULE TYPE: DNA (genomic)
317      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
319 CGCGGATCCG CCATCATGGT GCTGTGGGAG TCC      33
321 (2) INFORMATION FOR SEQ ID NO: 6:
323      (i) SEQUENCE CHARACTERISTICS:
324          (A) LENGTH: 31 base pairs
325          (B) TYPE: nucleic acid
326          (C) STRANDEDNESS: single
327          (D) TOPOLOGY: linear
329      (ii) MOLECULE TYPE: DNA (genomic)
334      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
336 GCGTCTAGAC TAGTATAGAA CACTGTAGTC C      31
338 (2) INFORMATION FOR SEQ ID NO: 7:
340      (i) SEQUENCE CHARACTERISTICS:
341          (A) LENGTH: 31 base pairs
342          (B) TYPE: nucleic acid
343          (C) STRANDEDNESS: single
344          (D) TOPOLOGY: linear
346      (ii) MOLECULE TYPE: DNA (genomic)
351      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
353 GCGTCTAGAC TAGTATAGAA CACTGTAGTC C      31
355 (2) INFORMATION FOR SEQ ID NO: 8:
357      (i) SEQUENCE CHARACTERISTICS:
358          (A) LENGTH: 31 base pairs
359          (B) TYPE: nucleic acid
360          (C) STRANDEDNESS: single
361          (D) TOPOLOGY: linear
363      (ii) MOLECULE TYPE: DNA (genomic)
368      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
370 GCGTCTAGAC TAGTATAGAA CACTGTAGTC C      31
372 (2) INFORMATION FOR SEQ ID NO: 9:
374      (i) SEQUENCE CHARACTERISTICS:

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VERIFICATION SUMMARYPATENT APPLICATION: **US/10/644,875**

DATE: 01/21/2004

TIME: 14:50:32

Input Set : **N:\Crf3\RULE60\10644875.RAW.txt**Output Set: **N:\CRF4\01212004\J644875.raw**

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:41 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:46 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]